S.Priebe ● ● 1632

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RAW SEQUENCE LISTING
PATENT APPLICATION   US/09/041,236

DATE: 12/03/98
TIME: 13:51:18

INPUT SET: S30140.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                                   SEQUENCE LISTING
 2
 3   (1)      General Information:
 4        (i) APPLICANT: Luo, Yuling
 5                       Xiomei, Xu
 6       (ii) TITLE OF INVENTION: Semaphorin K1
 7      (iii) NUMBER OF SEQUENCES: 4
 8       (iv) CORRESPONDENCE ADDRESS:
 9            (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
10            (B) STREET: 75 DENISE DRIVE
11            (C) CITY: HILLSBOROUGH
12            (D) STATE: CALIFORNIA
13            (E) COUNTRY: USA
14            (F) ZIP: 94010
15        (v) COMPUTER READABLE FORM:
16            (A) MEDIUM TYPE: Floppy disk
17            (B) COMPUTER: IBM PC compatible
18            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
19            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
20       (vi) CURRENT APPLICATION DATA:
21            (A) APPLICATION NUMBER:09/041,236
22            (B) FILING DATE:March 11, 1998
23            (C) CLASSIFICATION:
24     (viii) ATTORNEY/AGENT INFORMATION:
25            (A) NAME: OSMAN, RICHARD A
26            (B) REGISTRATION NUMBER: 36,627
27            (C) REFERENCE/DOCKET NUMBER: EXEL98-001
28       (ix) TELECOMMUNICATION INFORMATION:
29            (A) TELEPHONE: (650) 343-4341
30            (B) TELEFAX: (650) 343-4342
31
32   (2) INFORMATION FOR SEQ ID NO:1:
33        (i) SEQUENCE CHARACTERISTICS:
34            (A) LENGTH: 2498 base pairs
35            (B) TYPE: nucleic acid
36            (C) STRANDEDNESS: double
37            (D) TOPOLOGY: linear
38       (ii) MOLECULE TYPE: cDNA
39       (ix) FEATURE:
40            (A) NAME/KEY: CDS
41            (B) LOCATION: 1..1902
42       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
43   CTG CTG CTG CTG CTC TGG GCG GCC GCC GCC TCC GCC CAG GGC CAC CTA        48
44   Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
45     1               5                   10                  15
46   AGG AGC GGA CCC CGC ATC TTC GCC GTC TGG AAA GGC CAT GTA GGG CAG        96
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47  Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
48              20                  25                  30
49  GAC CGG GTG GAC TTT GGC CAG ACT GAG CCG CAC ACG GTG CTT TTC CAC    144
50  Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His
51          35                  40                  45
52  GAG CCA GGC AGC TCC TCT GTG TGG GTG GGA GGA CGT GGC AAG GTC TAC    192
53  Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr
54          50                  55                  60
55  CTC TTT GAC TTC CCC GAG GGC AAG AAC GCA TCT GTG CGC ACG GTG AAT    240
56  Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn
57  65                  70                  75                  80
58  ATC GGC TCC ACA AAG GGG TCC TGT CTG GAT AAG CGG GAC TGC GAG AAC    288
59  Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn
60                  85                  90                  95
61  TAC ATC ACT CTC CTG GAG AGG CGG AGT GAG GGG CTG CTG GCC TGT GGC    336
62  Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly
63              100                 105                 110
64  ACC AAC GCC CGG CAC CCC AGC TGC TGG AAC CTG GTG AAT GGC ACT GTG    384
65  Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val
66          115                 120                 125
67  GTG CCA CTT GGC GAG ATG AGA GGC TAC GCC CCC TTC AGC CCG GAC GAG    432
68  Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu
69          130                 135                 140
70  AAC TCC CTG GTT CTG TTT GAA GGG GAC GAG GTG TAT TCC ACC ATC CGG    480
71  Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg
72  145                 150                 155                 160
73  AAG CAG GAA TAC AAT GGG AAG ATC CCT CGG TTC CGC CGC ATC CGG GGC    528
74  Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly
75                  165                 170                 175
76  GAG AGT GAG CTG TAC ACC AGT GAT ACT GTC ATG CAG AAC CCA CAG TTC    576
77  Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe
78              180                 185                 190
79  ATC AAA GCC ACC ATC GTG CAC CAA GAC CAG GCT TAC GAT GAC AAG ATC    624
80  Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile
81          195                 200                 205
82  TAC TAC TTC TTC CGA GAG GAC AAT CCT GAC AAG AAT CCT GAG GCT CCT    672
83  Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro
84  210                 215                 220
85  CTC AAT GTG TCC CGT GTG GCC CAG TTG TGC AGG GGG GAC CAG GGT GGG    720
86  Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly
87  225                 230                 235                 240
88  GAA AGT TCA CTG TCA GTC TCC AAG TGG AAC ACT TTT CTG AAA GCC ATG    768
89  Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met
90                  245                 250                 255
91  CTG GTA TGC AGT GAT GCT GCC ACC AAC AAG AAC TTC AAC AGG CTG CAA    816
92  Leu Val Cys Ser Asp Ala Ala Thr Asn Lys Asn Phe Asn Arg Leu Gln
93                  260                 265                 270
94  GAC GTC TTC CTG CTC CCT GAC CCC AGC GGC CAG TGG AGG GAC ACC AGG    864
95  Asp Val Phe Leu Leu Pro Asp Pro Ser Gly Gln Trp Arg Asp Thr Arg
96          275                 280                 285
97  GTC TAT GGT GTT TTC TCC AAC CCC TGG AAC TAC TCA GCC GTC TGT GTG    912
98  Val Tyr Gly Val Phe Ser Asn Pro Trp Asn Tyr Ser Ala Val Cys Val
99          290                 295                 300
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PATENT APPLICATION *US/09/041,236*

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100   TAT TCC CTC GGT GAC ATT GAC AAG GTC TTC CGT ACC TCC TCA CTC AAG         960
101   Tyr Ser Leu Gly Asp Ile Asp Lys Val Phe Arg Thr Ser Ser Leu Lys
102   305                 310                 315                 320
103   GGC TAC CAC TCA AGC CTT CCC AAC CCG CGG CCT GGC AAG TGC CTC CCA        1008
104   Gly Tyr His Ser Ser Leu Pro Asn Pro Arg Pro Gly Lys Cys Leu Pro
105                       325                 330                 335
106   GAC CAG CAG CCG ATA CCC ACA GAG ACC TTC CAG GTG GCT GAC CGT CAC        1056
107   Asp Gln Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Arg His
108                       340                 345                 350
109   CCA GAG GTG GCG CAG AGG GTG GAG CCC ATG GGG CCT CTG AAG ACG CCA        1104
110   Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro
111                       355                 360                 365
112   TTG TTC CAC TCT AAA TAC CAC TAC CAG AAA GTG GCC GTC CAC CGC ATG        1152
113   Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met
114                       370                 375                 380
115   CAA GCC AGC CAC GGG GAG ACC TTT CAT GTG CTT TAC CTA ACT ACA GAC        1200
116   Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp
117   385                 390                 395                 400
118   AGG GGC ACT ATC CAC AAG GTG GTG GAA CCG GGG GAG CAG GAG CAC AGC        1248
119   Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser
120                       405                 410                 415
121   TTC GCC TTC AAC ATC ATG GAG ATC CAG CCC TTC CGC CGC GCG GCT GCC        1296
122   Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala
123                       420                 425                 430
124   ATC CAG ACC ATG TCG CTG GAT GCT GAG CGG AGG AAG CTG TAT GTG AGC        1344
125   Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser
126                       435                 440                 445
127   TCC CAG TGG GAG GTG AGC CAG GTG CCC CTG GAC CTG TGT GAG GTC TAT        1392
128   Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr
129         450                 455                 460
130   GGC GGG GGC TGC CAC GGT TGC CTC ATG TCC CGA GAC CCC TAC TGC GGC        1440
131   Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly
132   465                 470                 475                 480
133   TGG GAC CAA GGC CGC TGC ATC TCC ATC TAC AGC TCC GAA CGG TCA GTG        1488
134   Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val
135                       485                 490                 495
136   CTG CAA TCC ATT AAT CCA GCC GAG CCA CAC AAG GAG TGT CCC AAC CCC        1536
137   Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro
138                       500                 505                 510
139   AAA CCA GAC AAG GCC CCA CTG CAG AAG GTT TCC CTG GCC CCA AAC TCT        1584
140   Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser
141         515                 520                 525
142   CGC TAC TAC CTG AGC TGC CCC ATG GAA TCC CGC CAC GCC ACC TAC TCA        1632
143   Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser
144         530                 535                 540
145   TGG CGC CAC AAG GAG AAC GTG GAG CAG AGC TGC GAA CCT GGT CAC CAG        1680
146   Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln
147   545                 550                 555                 560
148   AGC CCC AAC TGC ATC CTG TTC ATC GAG AAC CTC ACG GCG CAG CAG TAC        1728
149   Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr
150                       565                 570                 575
151   GGC CAC TAC TTC TGC GAG GCC CAG GAG GGC TCC TAC TTC CGC GAG GCT        1776
152   Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala
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INPUT SET: S30140.raw

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153                 580              585               590
154     CAG CAC TGG CAG CTG CTG CCC GAG GAC GGC ATC ATG GCC GAG CAC CTG        1824
155     Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
156                 595              600               605
157     CTG GGT CAT GCC TGT GCC CTG GCC GCC TCC CTC TGG CTG GGG GTG CTG        1872
158     Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
159                 610              615               620
160     CCC ACA CTC ACT CTT GGC TTG CTG GTC CAC TAGGGCCTCC CGAGGCTGGG          1922
161     Pro Thr Leu Thr Leu Gly Leu Leu Val His
162     625                 630
163     CATGCCTCAG GCTTCTGCAG CCCAGGGCAC TAAAACGTCT CACACTCAGA GCCGGCTGGC      1982
164     CCGGGAGCTC CTTGCCTGCC ATTTTTTCCA GGGGACAGAA TAACCCAGTG GAGGATGCCA      2042
165     GGCCTGGAGA CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGTGGCGCAC GGATGGTGAG      2102
166     GGGCTGAGAA TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATTT      2162
167     TTTGGAAAAT ATTTTTCAGA CTCCTCAAAC TTGACTAAAT GCAGCGATGC TCCCAGCCCA      2222
168     AGAGCCCATG GGTCGGGGAG TGGGTTTGGA TAGGAGAGCT GGGATTCCAT CTCGACCCTG      2282
169     GGGCTGAGGC CTGAGTCCTT TTGGATTCTT GGTACCCACA TTGCCTCCTT CCCCTCCTTT      2342
170     TTTCAGGGGT GGGTGGTTGG TGTTCCTGAA GACCCAGGGA TACCCTTTGT CCAGCCCTGT      2402
171     CCTTGGCAGC TCCCTTTTTG GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG      2462
172     AAGGATGTTT GCTTTCCGGA CGGAAGGACG GAAAAA                                2498
173
174     (2) INFORMATION FOR SEQ ID NO:2:
175             (i) SEQUENCE CHARACTERISTICS:
176                     (A) LENGTH: 634 amino acids
177                     (B) TYPE: amino acid
178                     (D) TOPOLOGY: linear
179             (ii) MOLECULE TYPE: protein
180             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
181     Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
182     1               5               10              15
183     Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
184                 20              25              30
185     Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His
186             35              40              45
187     Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr
188         50              55              60
189     Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn
190     65              70              75              80
191     Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn
192                 85              90              95
193     Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly
194                 100             105             110
195     Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val
196             115             120             125
197     Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu
198         130             135             140
199     Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg
200     145             150             155             160
201     Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly
202                 165             170             175
203     Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe
204                 180             185             190
205     Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile
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206            195                    200                       205
207    Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro
208        210                    215                       220
209    Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly
210    225                    230                       235           240
211    Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met
212                245                    250                       255
213    Leu Val Cys Ser Asp Ala Ala Thr Asn Lys Asn Phe Asn Arg Leu Gln
214                260                    265                       270
215    Asp Val Phe Leu Leu Pro Asp Pro Ser Gly Gln Trp Arg Asp Thr Arg
216            275                    280                       285
217    Val Tyr Gly Val Phe Ser Asn Pro Trp Asn Tyr Ser Ala Val Cys Val
218        290                    295                       300
219    Tyr Ser Leu Gly Asp Ile Asp Lys Val Phe Arg Thr Ser Ser Leu Lys
220    305                    310                       315           320
221    Gly Tyr His Ser Ser Leu Pro Asn Pro Arg Pro Gly Lys Cys Leu Pro
222                325                    330                       335
223    Asp Gln Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Arg His
224                340                    345                       350
225    Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro
226            355                    360                       365
227    Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met
228        370                    375                       380
229    Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp
230    385                    390                       395           400
231    Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser
232                405                    410                       415
233    Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala
234                420                    425                       430
235    Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser
236            435                    440                       445
237    Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr
238        450                    455                       460
239    Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly
240    465                    470                       475           480
241    Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val
242                485                    490                       495
243    Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro
244                500                    505                       510
245    Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser
246            515                    520                       525
247    Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser
248        530                    535                       540
249    Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln
250    545                    550                       555           560
251    Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr
252                565                    570                       575
253    Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala
254                580                    585                       590
255    Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
256            595                    600                       605
257    Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
258        610                    615                       620
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/041,236*

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